

SEQUENCE LISTING

<110> Tanksley, Steven D.

<120> GENE CONTROLLING FRUIT SIZE AND CELL DIVISION IN PLANTS

<130> 19603/3211

<140>

<141>

<150> 60/215,824

<151> 2000-07-05

<160> 39

<170> PatentIn Ver. 2.1

<210> 1

<211> 492

<212> DNA

<213> Lycopersicon pennellii

<400> 1

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gatgacctgt ctaactgttt agttactagt gtttgccttt gtatcacctt tggacagatt 180
tctgaaatac taaacaaagg aacaacttca tgtgggagta gaggtgcatt atattgtttg 240
ctgggactga caggattgcc tagcctatat tctgtcttct acaggtctaa aatgaggggg 300
caatatgata tggaagaggc accttgtgtt gattgtcttg tacatgtatt ctgtgaacct 360
tgtgtctctt gccagaata cagagagctt aagaaccgtg gctttgatat ggggaatagg 420
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<210> 2

<211> 163

<212> PRT

<213> Lycopersicon pennellii

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1 5 10 15
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Val Pro Pro His Tyr Val Ser Ala Pro Gly Thr Thr Thr Ala Arg Trp
20 25 30
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<213> Lycopersicon esculentum

<400> 4

Met Tyr Gln Thr Val Gly Tyr Asn Pro Gly Pro Met Lys Gln Pro Tyr
1 5 10 15

Val Pro Pro His Tyr Val Ser Ala Pro Gly Thr Thr Thr Ala Arg Trp
20 25 30

Ser Thr Gly Leu Cys His Cys Phe Asp Asp Pro Ala Asn Cys Leu Val
35 40 45

Thr Ser Val Cys Pro Cys Ile Thr Phe Gly Gln Ile Ser Glu Ile Leu
50 55 60

Asn Lys Gly Thr Thr Ser Cys Gly Ser Arg Gly Ala Leu Tyr Cys Leu
65 70 75 80

Leu Gly Leu Thr Gly Leu Pro Ser Leu Tyr Ser Cys Phe Tyr Arg Ser
85 90 95

Lys Met Arg Gly Gln Tyr Asp Leu Glu Glu Ala Pro Cys Val Asp Cys
100 105 110

Leu Val His Val Phe Cys Glu Pro Cys Ala Leu Cys Gln Glu Tyr Arg
115 120 125

Glu Leu Lys Asn Arg Gly Phe Asp Met Gly Ile Gly Trp Gln Ala Asn
130 135 140

Met Asp Arg Gln Ser Arg Gly Val Thr Met Pro Pro Tyr His Ala Gly
145 150 155 160

Met Thr Arg

<210> 5

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: B26 Primer

<400> 5

gactcgagtc gacatcga

18

<210> 6
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: B25 Primer

<400> 6
 gactcgagtc gacatcga 18

<210> 7
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ORFXF2 Primer

<400> 7
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<210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FW01 Primer

<400> 8
 gcccttgat cacctttgga 20

<210> 9
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: GSP1 Primer

<400> 9
 gatgatttca ttgatcttgc a 21

<210> 10
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Abridged
 Anchor Primer

<220>
 <221> unsure
 <222> (24)..(35)
 <223> N at any position in this sequence is Inosine

<400> 10
 ggccacgcgt cgactagtagt gggnnngggnn gggngg 36

<210> 11
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: GSP2 Primer

<400> 11
 taacatgaac atgcaggag tc 22

<210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Abridged
 Universal Anchor Primer

<400> 12
 ggccacgcgt cgactagtagt 20

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GSP3 Primer

<400> 13

gggagtcgga gatagcattg

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<210> 14

<211> 164

<212> PRT

<213> Lycopersicon esculentum2

<400> 14

Met Asn Pro Ser Ala Gln Pro Ala Tyr Gly Glu Lys Pro Met Thr Gly
1 5 10 15

Val Pro Val Pro Gly Gln Phe Gln Ala Asn His Pro Gly Asn Trp Ser
20 25 30

Thr Gly Leu Cys Asp Cys Phe Ser Asp Ile Ser Ser Cys Cys Leu Thr
35 40 45

Cys Trp Cys Pro Cys Ile Thr Phe Gly Gln Ile Ala Glu Ile Val Asp
50 55 60

Lys Gly Thr Val Ser Cys Gly Ala Ser Gly Ala Leu Tyr Phe Leu Ile
65 70 75 80

Glu Ala Leu Thr Gly Cys Gly Cys Ile Tyr Ser Cys Phe Tyr Arg Ile
85 90 95

Lys Met Arg Lys Gln Tyr Met Leu Pro Glu Ser Pro Cys Gly Asp Cys
100 105 110

Leu Leu His Phe Cys Cys Glu Cys Cys Ala Leu Cys Gln Glu His Arg
115 120 125

Glu Leu Lys His Arg Gly Tyr Asp Met Ser Ile Gly Trp Gln Gly Asn
130 135 140

Met Asp Asn Gln Asn Gly Gly Ile Ala Met Ala Pro Gly Val Gln Gly
145 150 155 160

Gly Met Thr Arg

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

Trp Ser Thr Gly Leu Cys Asp Cys Met Ser Asp Pro Lys Asn Cys Cys
20 25 30

Ile Thr Leu Trp Cys Pro Cys Ile Thr Phe Gly Gln Val Ala Glu Ile
35 40 45

Ile Asp Lys Gly Ser Asn Ser Cys Gly Val Asn Gly Ala Leu Tyr Thr
50 55 60

Ile Ile Ile Cys Val Thr Ser Cys Pro Cys Ile Tyr Ser Cys Phe Tyr
65 70 75 80

Arg Asn Lys Met Arg Gln Gln Tyr Leu Leu Lys Lys Ser Pro Cys Gly
85 90 95

Asp Cys Leu Val His Cys Phe Trp Glu Ala Cys Ala Leu Cys Gln Glu
100 105 110

Tyr Arg Glu Leu Lys Asn Gln Gly Val Asp Met Ser Ile Gly Trp His
115 120 125

Gly Asn Val Glu Arg Gln
130

<400> 16
Met Gly Met Gly Gln Tyr Gln Gln Gly Met Gln Pro Ala Pro Pro Met
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Met Gly Ile Pro Phe Lys Pro Ile Leu Pro Thr Glu Ser Trp Lys Thr
20 25 30

Gly Leu Phe Asp Cys Met Glu Asp Pro Thr Asn Ala Leu Ile Thr Ala
35 40 45

85

90

95

Met Pro Ala Val Cys Ser Gln Trp Ile Met Gly Ser Lys Tyr Arg Thr
100 105 110

Gln Leu Arg Gln Arg Tyr Asn Leu Val Glu Ala Pro Tyr Ser Asp Met
115 120 125

Ile Ser His Met Phe Cys Pro Cys Gly Ser Leu Cys Gln Glu Phe Arg
130 135 140

Glu Leu Leu Asn Arg Gly Leu Asp Pro Ala Leu Gly Trp Asn Gly Ile
145 150 155 160

Val Ala Gln Arg His Tyr Gly Asn Gln Gln Val Asn Gln Ala Ser
165 170 175

<210> 18

<211> 145

<212> PRT

<213> Petunia hybrida

<400> 18

Met Ser Asp Arg Pro Gln Val Pro Trp Ser Ser Gly Ile Cys Asp Cys
1 5 10 15

Phe Gln Asp Val Lys Gly Cys Cys Leu Thr Cys Trp Cys Pro Cys Ile
20 25 30

Thr Phe Gly Arg Ile Ala Glu Val Ala Asp Gln Gly Ser Thr Ser Cys
35 40 45

Val Val Ser Gly Thr Val Tyr Leu Leu Val Tyr Leu Val Thr Ser Gly
50 55 60

Phe Gly Cys Cys Trp Tyr Ser Cys Phe Tyr Arg Ser Lys Leu Arg Asn
65 70 75 80

Gln Tyr Tyr Leu Asp Glu Lys Pro Cys Ser Asp Leu Cys Thr His Cys
85 90 95

Cys Cys Glu Tyr Cys Ala Leu Cys Gln Glu Tyr Arg Glu Leu Gln Asn
100 105 110

Gln Gly Phe Asp Met Ser Thr Gly Trp Asn Glu Asn Met Glu Lys Trp
115 120 125

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<400> 20

Met Glu Ala Gln His Leu His Ala Lys Pro His Ala Glu Gly Glu Trp
1 5 10 15

Ser Thr Gly Phe Cys Asp Cys Phe Ser Asp Cys Lys Asn Cys Cys Ile
20 25 30

Thr Phe Trp Cys Pro Cys Ile Thr Phe Gly Gln Val Ala Glu Ile Val
35 40 45

Asp Arg Gly Ser Thr Ser Cys Gly Thr Ala Gly Ala Leu Tyr Ala Leu
50 55 60

Ile Ala Val Val Thr Gly Cys Ala Cys Ile Tyr Ser Cys Phe Tyr Arg
65 70 75 80

Gly Lys Met Arg Ala Gln Tyr Asn Ile Lys Gly Asp Asp Cys Thr Asp
85 90 95

Cys Leu Lys His Phe Cys Cys Phe Leu Cys Ser Leu Thr Gln Gln Tyr
100 105 110

Arg Glu Leu Lys His Arg Gly Tyr Asp Met Ser Leu Gly Trp Ala Gly
115 120 125

Asn Val Glu Arg Gln Gln Asn Gln Gly Gly Val Ala Met Gly Ala Pro
130 135 140

Val Phe Gln Gly Gly Met Thr Arg
145 150

<210> 21

<211> 151

<212> PRT

<213> Arabidopsis thaliana2b

<400> 21

Met Glu Ala Gln Leu His Ala Lys Pro His Ala Gln Gly Glu Trp Ser
1 5 10 15

Thr Gly Phe Cys Asp Cys Phe Ser Asp Cys Arg Asn Cys Cys Ile Thr
20 25 30

Leu Cys Cys Pro Cys Ile Thr Phe Gly Gln Val Ala Glu Ile Val Asp
35 40 45

Pro Ser Ile Ser Gly Trp Ser Gly Asn Met Gln Arg Thr Met Ala Pro
115 120 125

Pro Met Ser Gln Gln Met Met Gly
130 135

<210> 23

<211> 190

<212> PRT

<213> Arabidopsis thaliana3b

<400> 23

Met Gly Arg Pro Gly Ser Gln Pro Asn Glu Ala Gln Pro Pro Pro Val
1 5 10 15

Gln Val Gln Pro Thr Val Asn Arg Asp Asn Gln Val His Ser Gln Asn
20 25 30

Gly Ala Ile Gly Gln Ala Asn Ile Gln Thr Gly Arg Pro Val Asn Asn
35 40 45

Gln Thr Gln Asn Leu Trp Ser Ser Asp Leu Phe Asp Cys Met Asn Asp
50 55 60

Ser Glu Asn Gly Leu Cys Ile Gly Ser Ala Val Ile Thr Cys Leu Ala
65 70 75 80

Pro Cys Val Thr Leu Gly Gln Ile Ala Glu Ile Val Asp Glu Gly Ala
85 90 95

Thr Thr Cys Ala Thr Gly Gly Leu Leu Tyr Gly Met Ile Phe Phe Ile
100 105 110

Gly Val Pro Phe Val Tyr Ser Cys Met Phe Arg Ala Lys Met Arg Asn
115 120 125

Lys Tyr Gly Leu Pro Asp Ala Pro Ala Pro Asp Trp Ile Thr His Leu
130 135 140

Phe Cys Glu His Cys Ala Leu Cys Gln Glu Tyr Arg Glu Leu Lys His
145 150 155 160

Arg Gly Phe Asp Pro Asn Ile Gly Trp Ala Gly Asn Val Gln Ala Gln
165 170 175

Gln Pro Val Met Ser Pro Pro Thr Gly Gln Arg Met Met Gly

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<212> PRT

<213> Arabidopsis thaliana4a

<400> 25

Met Tyr Gly Asn Gly Pro Val Phe Lys Ala Glu Gly Thr Ser Phe Arg
1 5 10 15

Asp Gln Pro Tyr Ala Glu Gln Leu Pro Gln Gly Leu Trp Thr Thr Gly
20 25 30

Leu Cys Asp Cys His Glu Asp Ala His Ile Cys Thr Tyr Gln Asn Thr
35 40 45

Ala Ile Met Pro Cys Val Ser Phe Ala Gln Asn Val Glu Ile Val Asn
50 55 60

Arg Gly Thr Ile Thr Cys Met Asn Ala Gly Leu Ile His Leu Ala Leu
65 70 75 80

Gly Phe Ile Gly Cys Ser Trp Leu Tyr Ala Phe Pro Asn Arg Ser Arg
85 90 95

Leu Arg Glu His Phe Ala Leu Pro Glu Glu Pro Cys Arg Asp Phe Leu
100 105 110

Val His Leu Phe Cys Thr Pro Cys Ala Ile Cys Gln Glu Ser Arg Glu
115 120 125

Leu Lys Asn Arg Gly Ala Asp Pro Ser Ile Gly Trp Leu Ser Asn Val
130 135 140

Glu Lys Trp Ser Arg Glu Lys Val Thr Pro Pro Ile Val Val Pro Gly
145 150 155 160

Met Ile Arg

<210> 26

<211> 160

<212> PRT

<213> Arabidopsis thaliana4b

<400> 26

Met Asn Leu Ser Ser Asn Asp Gln Pro Ser Gln Gly Arg Ile Lys Ala
1 5 10 15

Lys Asp Trp Ser Thr Asp Leu Cys Glu Cys Trp Met Asp Ile Asn Ser

45

Gly Lys Met Arg Ala Gln Tyr Asn Ile Lys Gly Asp
100 105

Arg Pro Lys Met Arg Arg Gln Tyr Gly Leu Lys Gly Asn Gly Cys Ser

115

120

125

Asp Cys Leu Ile His Cys Phe Cys Glu Pro Cys Ala Leu Cys Gln Glu
 130 135 140

Tyr Arg Glu Leu Gln His Arg Gly Phe Asp Met Ile Ile Xaa Trp His
 145 150 155 160

Gly Asn Val Glu Gln Arg Ser
 165

<210> 29

<211> 72

<212> PRT

<213> Glycine max2

<400> 29

Arg Ala Glu Phe Gly Thr Arg Phe Ala Ala Ala Cys Gly Ala Ser Gly
 1 5 10 15

Ala Leu Tyr Thr Leu Ile Cys Cys Val Ile Gly Cys Gly Cys Leu Tyr
 20 25 30

Ser Cys Phe Tyr Arg Pro Lys Met Arg Arg Gln Tyr Gly Leu Lys Gly
 35 40 45

Asn Gly Cys Ser Asp Cys Leu Ile His Cys Phe Cys Glu Pro Cys Ala
 50 55 60

Leu Cys Gln Glu Tyr Arg Glu Leu
 65 70

<210> 30

<211> 138

<212> PRT

<213> O.sativai

<220>

<221> UNSURE

<222> (138)

<223> Xaa at position 138 in this sequence is unknown

<400> 30

Met Gln Asp Gln Ala Ala Pro Val Pro Trp Ser Thr Asp Leu Phe Asp
 1 5 10 15

Met Arg Gly Arg Val Thr Lys Pro Ala Met Thr Met Pro Pro His Met
 100 105 110

Phe Pro Gly Met Asp Thr Leu Ile Asp Ser Lys
 115 120

<210> 32

<211> 103

<212> PRT

<213> O.sativa3

<400> 32

Gly Thr Cys Pro Cys Leu Ala Ser Gly Thr Ala Tyr Ala Leu Leu Cys
 1 5 10 15

Ala Ser Gly Met Gly Cys Leu Tyr Ser Cys Phe Tyr Arg Ser Lys Met
 20 25 30

Arg Ala Gln Phe Asp Leu Asp Glu Gly Asp Cys Pro Asp Phe Leu Val
 35 40 45

His Phe Cys Cys Glu Tyr Cys Ala Leu Cys Gln Glu Tyr Arg Glu Leu
 50 55 60

Lys Asn Arg Gly Phe Asp Leu Gly Ile Gly Trp Ala Ala Asn Val Asp
 65 70 75 80

Arg Gln Arg Arg Gly Val Thr Gly Ala Ser Val Met Gly Ala Pro Gly
 85 90 95

Val Pro Val Gly Met Met Arg
 100

<210> 33

<211> 135

<212> PRT

<213> O.sativa4

<400> 33

Asn Lys Gly Leu Tyr Ser Gln Ala Met Tyr Pro Ser Ala Pro Pro Asp
 1 5 10 15

Ala Tyr Asn Lys Tyr Ser Ala Gly Ala Pro Pro Thr Ala Pro Pro Pro
 20 25 30

Ala Thr Tyr Gln Leu Pro Thr Met Asn Thr Pro Arg Thr Gly Gly Gly
35 40 45

Leu Thr Arg Trp Ser Thr Gly Leu Phe His Cys Met Asp Asp Pro Gly
50 55 60

Asn Cys Leu Ile Thr Cys Val Cys Pro Cys Ile Thr Phe Gly Gln Val
65 70 75 80

Ala Asp Ile Val Asp Lys Gly Thr Cys Pro Cys Leu Ala Ser Gly Thr
85 90 95

Ala Tyr Ala Leu Leu Cys Ala Ser Gly Met Gly Cys Leu Tyr Ser Cys
100 105 110

Phe Tyr Arg Ser Lys Met Arg Ala Gln Phe Asp Leu Asp Glu Gly Asp
115 120 125

Cys Pro Asp Phe Leu Val His
130 135

<210> 34

<211> 81

<212> PRT

<213> O.sativa5

 $\langle 220 \rangle$

<221> UNSURE

 $\langle 222 \rangle$ (10) . . (61)

<223> Xaa at any position in this sequence is unknown

<400> 34

Leu Tyr Ser Cys Phe Tyr Arg Ser Lys Xaa Arg Ala Gln Phe Asp Leu
1 5 10 15

Asp Glu Gly Asp Cys Pro Asp Phe Leu Val His Phe Cys Cys Glu Tyr
20 25 30

Cys Ala Leu Cys Gln Glu Tyr Arg Glu Leu Lys Asn Arg Gly Phe Asp
35 40 45

Leu Gly Ile Gly Trp Ala Xaa Asn Val Asp Arg Gln Xaa Arg Gly Val
50 55 60

Thr Gly Ala Ser Val Met Gly Ala Pro Gly Val Pro Val Gly Met Met
65 70 75 80

Ser Cys His Phe Ile Met Ser Met His Asp Ser Ile Pro Gly Cys Leu
1 5 10 15

Thr Cys Trp Cys Pro Cys Ile Thr Phe Gly Arg Val Pro Glu Ile Val
20 25 30

Asp Xaa Gly Ala Thr Ser Cys Gly Thr Ala Gly Ala Leu Tyr Pro Val
35 40 45

Leu Ala Tyr Phe Pro Gly Cys Gln Trp Ile Tyr Ser Cys Thr Tyr Arg
50 55 60

Ala Lys Met Arg Ala Gln Leu Gly Leu Pro Glu Thr Pro Cys Cys Asp
65 70 75 80

Cys Leu Val His Phe Cys Cys Glu Pro Cys Ala Leu Cys Gln Gln Tyr
85 90 95

Lys Glu Leu Lys Ala Arg Gly Phe Asp Pro Val Leu Gly Trp Asp Arg
100 105 110

Asn Ala Thr Met Leu Pro Pro Ser Ala Gln Gly Met Gly Arg
115 120 125

<210> 38

<211> 63

<212> PRT

<213> Zea mays2

<220>

<221> UNSURE

<222> (26) .. (27)

<223> Xaa at positions 26 and 27 are unknown

<400> 38

Pro Thr Ile Thr Val Lys Met Ser Thr Tyr Pro Pro Pro Thr Gly Glu
1 5 10 15

Trp Thr Thr Gly Leu Cys Gly Cys Phe Xaa Xaa Cys Lys Ser Cys Cys
20 25 30

Leu Ser Phe Leu Cys Pro Cys Ile Pro Phe Gly Gln Val Ala Glu Val
35 40 45

Leu Asp Lys Gly Met Thr Ser Cys Gly Leu Ala Gly Leu Leu Tyr
50 55 60

[illegible]

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06987-03

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